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In the Claims:

Please amend claims 73 and 81 as follows:

73. (Amended) A method for detecting the presence of [a polypeptide of claim 67 in a sample, comprising:] a polypeptide having an amino acid sequence selected from the group consisting of:

[(a) contacting the sample with a compound which selectively binds to a polypeptide of claim 67; and

(b) determining whether the compound binds to the polypeptide in the sample.]

(a) the amino acid sequence shown in SEQ ID NO:1;

(b) the amino acid sequence encoded by the cDNA contained in ATCC

Deposit No. PTA-2369;

(c) the amino acid sequence of an allelic variant of the amino acid sequence shown in SEQ ID NO:1;

(d) the amino acid sequence of an allelic variant of the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369;

(e) a fragment of a polypeptide comprising the amino acid sequence of SEQ ID NO:1, or an amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:1, or an amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369;

(f) a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:1, or an amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369; wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a nucleic acid comprising SEQ ID NO:2, or a complement thereof under stringent conditions; and

(g) a polypeptide which is encoded by a nucleic acid molecule comprising a

C2 nucleotide sequence which is at least 45% identical to a nucleic acid comprising the nucleotide sequence of SEQ ID NO:2, or a complement thereof;

said method comprising contacting the sample with a compound which selectively binds to any one of the polypeptides of (a) – (g) and determining whether the compound binds to said polypeptides in the sample.

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81.(Amended) A method for modulating the activity of [a polypeptide of claim 67] a polypeptide having an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence shown in SEQ ID NO:1;

(b) the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369;

(c) the amino acid sequence of an allelic variant of the amino acid sequence shown in SEQ ID NO:1;

C3 (d) the amino acid sequence of an allelic variant of the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369;

(e) a fragment of a polypeptide comprising the amino acid sequence of SEQ ID NO:1, or an amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:1, or an amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369;

(f) a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:1, or an amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369; wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a nucleic acid comprising SEQ ID NO:2, or a complement thereof under stringent conditions; and

(g) a polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 45% identical to a nucleic acid comprising the nucleotide sequence of SEQ ID NO:2, or a complement thereof;